ABSTRACT

THESIS: New Antibiotic Discovery from Dairy Environments

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Each year globally, the rise of antimicrobial resistant bacterial infections becomes more pressing in modern clinical and agricultural systems, as genetic variation in pathogenic bacteria evolves at an increasingly rapid rate. The causes of this crisis are due to overuse and misuse of antibiotics, both in the clinical and agricultural environments, which expedite bacterial adaptation to the selective pressure of antibiotic exposure. Our lab is entering into a new research direction, in order to search for bacterial products (secondary metabolites) with promise as possible antimicrobial agents, through the analysis of various dairy farm environmental samples. The dairy environment is a relatively unexplored arena in this regard, and is home to many species of known and unknown microorganisms that could potentially show measurable antimicrobial activity against pathogenic bacteria. To screen for novel antibiotics, we first isolated bacterial cultures from raw (bovine) milk, manure, corn silage, trough water, and soil. Diluted samples were plated on 50% tryptic soy agar (TSA) plates, and further examined for antagonistic activity against a battery of pathogens (ESKAPE group). After screening approximately 30,000 bacterial isolates, we isolated and identified four bacterial isolates that

showed a reproducible zone of inhibition against at least one of four of our antimicrobial resistant pathogens. Lastly, we tentatively identified the genus of each of the unknown isolates through biochemical profiling. These results suggest that microorganisms from the dairy environment have the potential to produce secondary metabolites, leaving the door open to further purify the respective antimicrobial compound from each dairy farm isolate, and to identify each to the species level using 16S rDNA and ITS sequence analysis. These results may lead to the availability of a novel antibiotics in an era when little attention is being given to this global crisis.